Amendments to the Specification:

Please replace the paragraph immediately following the title, with the following amended paragraph:

This application is a section 371 application of PCT/EP2004/053594, filed December 17, 2004, which claims the benefit under 35 U.S.C. §119(e) of U.S. Provisional Application 60/531,866, filed December 22, 2003.

Please replace paragraph [0028] of the specification (published application 20070118931) with the following amended paragraph:

[0028] Methods for the search and identification of GRUBX homologues would be well within the realm of persons skilled in the art. Such methods comprise comparison of the sequences represented by SEQ ID NO 1 or 2, in a computer readable format, with sequences that are available in public databases such as MIPS (Munich Information Center for Protein Sequences, ~~http://~~mips.gsf.de/), GenBank (~~http://www.~~ncbi.nlm.nih.gov/Genbank/index.html) or EMBL Nucleotide Sequence Database (~~http://www.~~ebi.ac.uk/embl/index.html), using algorithms well known in the art for the alignment or comparison of sequences, such as GAP (Needleman and Wunsch, J. Mol. Biol. 48, 443-453 (1970)), BESTFIT (using the local homology algorithm of Smith and Waterman (Advances in Applied Mathematics 2, 482-489 (1981))), BLAST (Altschul, S. F., Gish, W., Miller, W., Myers, E. W. & Lipman, D. J., J. Mol. Biol. 215, 403-410 (1990)), FASTA and TFASTA (W. R. Pearson and D. J. Lipman Proc. Natl. Acad. Sci. USA 85, 2444-2448 (1988)). The software for performing BLAST analysis is publicly available through the National Centre for Biotechnology Information. The abovementioned homologues were identified using blast default parameters (for example BLASTN Program Advanced Options: G-Cost (to open a gap)=5; E-Cost (to extend a gap)=2; q-Penalty (for a mismatch)=-3; r-Reward (for a match)=1; e-Expectation value (E)=10.0; W-Word size=11; TBLASTN Program Advanced Options: G-Cost (to open a gap)=11; E-Cost (to extend a gap)=1; e-Expectation value (E)=10.0; W-Word size=3). As more genomes are being sequenced, it is expected that many more GRUBX homologues will be identifiable.

Please replace paragraph [0153] of the specification (published application 20070118931) with the following amended paragraph:

[0153] A c-DNA library with an average size of inserts of 1,400 bp was prepared from poly(A.sup.+) RNA isolated from actively dividing, non-synchronized BY2 tobacco cells. These library-inserts were cloned in the vector pCMVSPORT6.0, comprising an attB Gateway cassette (Life Technologies). From this library, 46,000 clones were selected, arrayed in 384-well microtiter plates, and subsequently spotted in duplicate on nylon filters. The arrayed clones were screened using pools of several hundreds of radioactively labelled tags as probes (including the BY2-tag corresponding to the sequence CDS0669, SEQ IDNO 1). Positive clones were isolated (among which the done corresponding to CDS0669, SEQ I NO 1), sequenced, and aligned with the tag sequence. Where the hybridisation with the tag failed, the full-length cDNA corresponding to the tag was selected by PCR amplification: tag-specific primers were designed using primer3 program (~~http://www-~~genome.wi.mit.edu/genome software/other/primer3.html) and used in combination with a common vector primer to amplify partial cDNA inserts. Pools of DNA from 50,000, 100,000, 150,000, and 300,000 cDNA clones were used as templates in the PCR amplifications. Amplification products were then isolated from agarose gels, cloned, sequenced and their sequence aligned with those of the tags. Next, the full-length cDNA corresponding to the nucleotide sequence of SEQ ID NO 1 was cloned from the pCMVsport6.0 library vector into pDONR201, a Gateway.RTM. donor vector (Invitrogen, Paisley, UK) via a LR reaction, resulting in the entry clone p77 (FIG. 3).